IN THE ABSTRACT:

Please DELETE the Abstract in its entirety and substitute the attached new Abstract.

An equivalence relationship is created between a) the functional network of the genome and proteome and b) a neuronal network. Both networks represent highly cross-linked feedback systems. The equivalence relationship makes it possible to model the functional network of proteins of and genes by an equivalent artificial neuronal network. The dynamic interaction of genes and regulatory proteins is modeled by a dynamic neuronal network. The method uses information obtained in a temporal sequence of gene expression patterns for identification of causal regulatory correlations, thereby enabling target proteins to be identified on a systematic basis.